MinION™ sequencing of the *Leishmania infantum* genome

Roger Farrés Catalán

Faculty of Veterinary Medicine – Final degree project, June 2020

Introduction

- The MinION™ is a portable, innovative, long reads sequencing device based on Nanopore technology
- Nanopore characteristics could be useful to decipher some *Leishmania infantum* genome attributes and simplify processes
- Still not used on complete *Leishmania* genome sequencing

Objectives

- Prove MinION™ capability to sequence the complex genome of *Leishmania infantum*
- Analyze and discuss the advantages and possibilities of the method

Results

Table 1. Comparison of the previous assemblies of the *L. infantum* genome and the present project

	Peacock (2007)[1]	Gonzalez de la Fuente (2017)[2]	Present project
Technique	Sanger	Illumina + PacBio	Nanopore
Fragments	470 (36 chromosomes)	36 (85*)	68
%GC	59,3	59,54	59,49
Genome size (pb)	32.134.935	32.802.969	33.186.418
Larger *chromosome* (pb)	2.673.956	2.743.073	2.745.455
Coverage	x5	x100	x64

* Total fragments before discards

Conclusions

- First precedent of complete *Leishmania infantum* genome sequencing with MinION that opens up several avenues of research with potential clinical applications[3]
- Accurate sequencing and assembly can be achieved with a simple and short procedure
- Assembly polishment could be done to improve the quality of the results

Methods

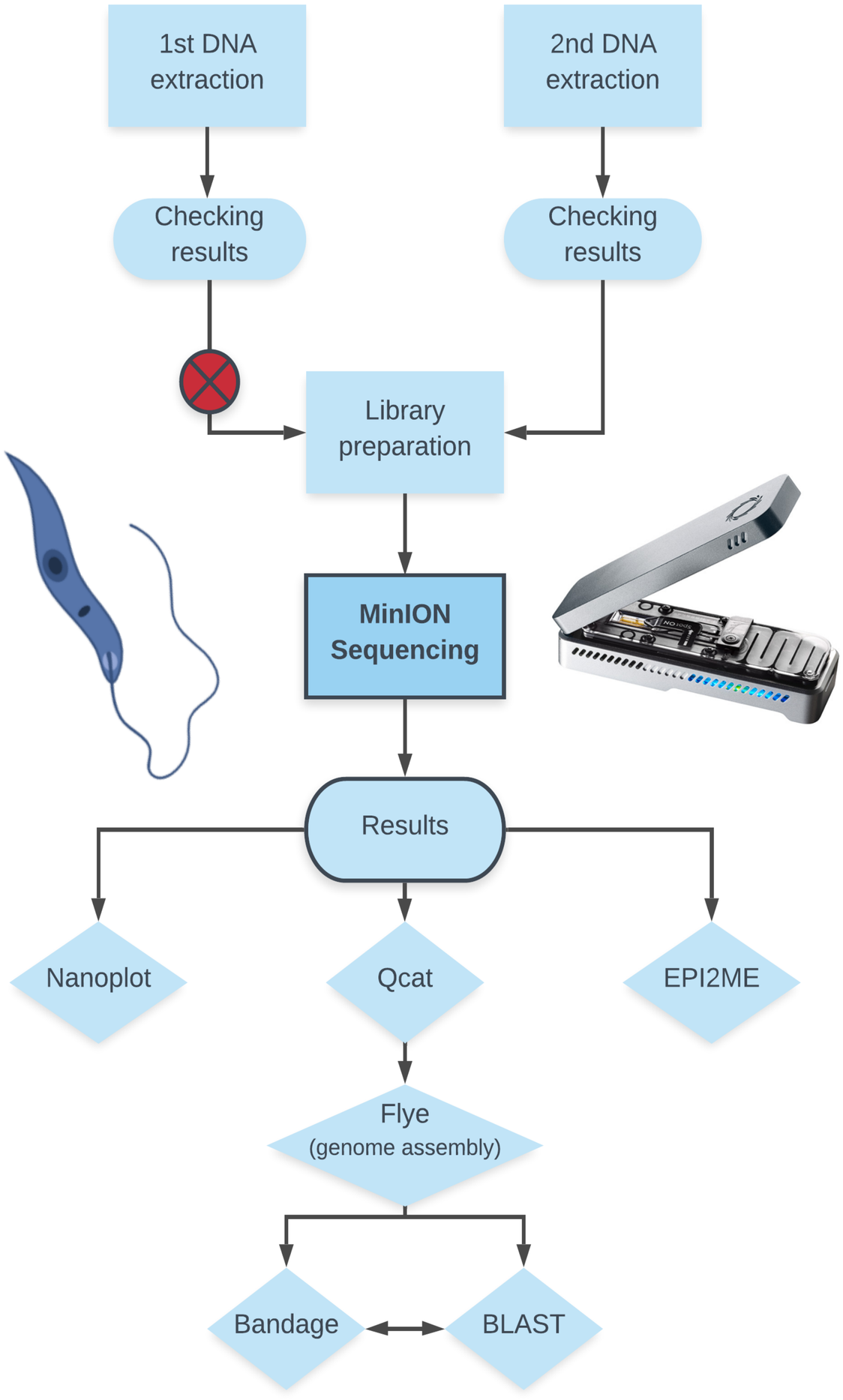

Figure 1. Methods used in the practical part of the project

Main references:

1. Peacock CS, Seeger K, Harris D, Murphy L, Ruiz JC, Quail MA, Peters N, Adlem E, Tivey A, Aslett M, et al. 2007. Comparative genomic analysis of three Leishmania species that cause diverse human disease. Nat Genet.
2. González-De La Fuente S, Camacho E, Peiró-Pastor R, Rastrojo A, Carrasco-Ramiro F, Aguado B, Requena JM. 2019. Complete and de novo assembly of the Leishmania braziliensis (M2904) genome. Mem Inst Oswaldo Cruz.
3. Imai K, Tarumoto N, Amo K, Takahashi M, Sakamoto N, Kosaka A, Kato Y, Mikita K, Sakai J, Murakami T, et al. 2018. Non-invasive diagnosis of cutaneous leishmaniasis by the direct boil loop-mediated isothermal amplification method and MinION™ nanopore sequencing. Parasitol Int.